



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96722

TO: Sheela Huff
Location: CM1/8B07/8E12
Art Unit: 1642
Sunday, June 22, 2003

Case Serial Number: 830811

From: Mary Jane Ruhl
Location: Biotech-Chem Library
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Search Notes

WO 0117557

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
c	c	1	18	100.0	2625	A83536 AX03786 Sequence 1
c	c	2	18	100.0	2625	6 AX03786 Sequence 1
c	c	3	18	100.0	2625	6 134433 Sequence 57
c	c	4	18	100.0	2625	6 146831 Sequence 51
c	c	5	18	100.0	2625	6 155100 Sequence 57
c	c	6	18	100.0	2625	6 HUMC11A
c	c	7	18	100.0	3440	9 BC013609 Homo sapi
c	c	8	18	100.0	3661	9 HUMOSF4A
c	c	9	18	100.0	3712	6 AR034822 Sequence
c	c	10	18	100.0	3712	6 E07302 Sequence
c	c	11	18	100.0	3867	9 HUMOSF4B
c	c	12	18	100.0	3914	6 AR034823 Sequence
c	c	13	18	100.0	3914	6 E07383 Sequence
c	c	14	18	100.0	153588	9 AC010533 Homo sapi
c	c	15	18	100.0	188894	2 AC086556 Homo sapi
c	c	16	18	100.0	194690	9 AC025763 Homo sapi
c	c	17	15	91.1	3180	MUSC11
c	c	18	16	91.1	3489	10 MUSOSF4
c	c	19	16	91.1	3581	6 AR034821 Sequence
c	c	20	16	91.1	4127	6 E07381 Sequence
c	c	21	16	91.1	4127	6 AX306074 Sequence
c	c	22	16	91.1	4127	10 MMCADE Sequence
c	c	23	16	91.1	64379	2 AC113037 Mus musculus
c	c	24	16	91.1	106376	9 AL138714 Human DNA
c	c	25	16	91.1	118327	9 HSD18B1
c	c	26	16	91.1	15192	2 AC123048 Sequence
c	c	27	16	91.1	170453	9 AC005600 Homo sapi
c	c	28	16	91.1	173556	9 AR074388 Homo sapi
c	c	29	16	91.1	176625	9 AC015977 Homo sapi
c	c	30	16	91.1	176638	9 AL590312 Homo sapi
c	c	31	16	91.1	178549	2 AC105962 Rattus norvegicus
c	c	32	16	91.1	20594	2 AL355373 Homo sapi
c	c	33	16	91.1	207212	2 AL671708 Homo sapi
c	c	34	16	88.9	4520	8 DR8669 Btryopsis clarkii
c	c	35	15	85.6	345	6 AX14171 Sequence
c	c	36	15	85.6	1206	6 AK027308 Homo sapi
c	c	37	15	85.6	1522	9 BC001611 Homo sapi
c	c	38	15	85.6	1695	10 RNNU6936 U56936 Rattus norvegicus
c	c	39	15	85.6	2137	9 AF231969 Homo sapi
c	c	40	15	85.6	2210	9 HSA211801 Homo sapi
c	c	41	15	85.6	2213	9 AF152694 Homo sapi
c	c	42	15	85.6	2307	6 AR116594 Sequence
c	c	43	15	85.6	3268	1 AF269352 Staphylococcus aureus
c	c	44	15	85.6	3268	1 AX146762 Sequence
c	c	45	15	85.6	3268	1 AE001050 Archaeopteryx

ALIGNMENTS

RESULT 1
 A8336/c
 LOCUS A83536
 DEFINITION Sequence 1 from Patent WO9849560.
 ACCESSION A83536
 VERSION A83536.1 GI:6732796
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE unclassified.
 1 (bases 1 to 2625)
 AUTHORS MacCallum, C.D. and Stephenson, M.D.
 TITLE CADHERIN-11 AS AN INDICATOR OF VIABLE PREGNANCY

Pred. NO. is the number of results predicted by chance to have a

FEATURES	source	Location/Qualifiers		VERSION	134433.1	GT:1825224
BASE COUNT	730 a	<i>/organism="unidentified"</i> <i>/db_xref="Taxon:32644"</i>		KEYWORDS	Unknown.	
ORIGIN	661 c	675 g		ORGANISM	Unclassified.	
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Best Local Similarity	100.0%	Pred. No. 41; Matches 18; Conservative 18; Mismatches 0; Indels 0; Gaps 0;		AUTHORS	Suzuki,S.	
DEFINITION	Sequence 1 from Patent WO0117557.	DNA		TITLE	Cadherin-specific antibodies and hybridoma cell lines	
ACCESSION	AX093786	linear		JOURNAL	PATENT: US 5597725-A 57 20-JAN-1997;	
VERSION	AX093786.1	PAT 30-MAR-2001		FEATURES	Location/Qualifiers	
KEYWORDS	human.	<i>/organism="unknown"</i>		SOURCE	I. .2625	
SOURCE	ORGANISM	homo sapiens		BASE COUNT	730 a	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	REFERENCE	AX093786		ORIGIN	661 c	
I. (bases 1 to 2625)	AUTHORS	Brenner,M.B. and Valencia,X.		Query Match	100.0%	
Methods and compositions for treatment of inflammatory disease using cadherin-11 modulating agents	TITLE	Patent: WO 0117557-A 15-MAR-2001;		Best Local Similarity	100.0%	
JOURNAL	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)	Location/Qualifiers		Matches	18	
FEATURES	source	I. .2625		ACCESSION	146831	
source	ORGANISM	<i>/organism="Homo sapiens"</i>		DEFINITION	Sequence 51 from patent US 5639534.	
/db_xref="taxon:9606"	REFERENCE	I. (bases 1 to 2625)		VERSION	146831.1	
156. .2546	AUTHORS	Suzuki,S.		JOURNAL	G1:2470796	
/note= "unnamed protein product"	TITLE	Cadherin polynucleotides		FEATURES	Unknown.	
/codon_start=1	DEFINITION	Patent: US 5639534-A 51 17-JUN-1997;		SOURCE	Unclassified.	
/protein_id=CAC35421.1"	ACCESSION	I. .2625		BASE COUNT	730 a	
/db_xref="G1:1351050"	REFERENCE	<i>/organism="unknown"</i>		ORIGIN	661 c	
/translation="MKENYCLQALVCLGMCHASHAFAPERRGLRSPFHGEKKE GOVQYEGGSVAGSLSLSESITSDDLDYLQWMPREKKLADLYSKDTPDDDS"	AUTHORS	675 g		Query Match	100.0%	
IDKGSGNTHAKLDRERQAQTLMQAVIDRNTNPLEPSEPTVKQVDINNPBPETL HETYHANPPERSKVGTSTQTAASDAPPYGNKAQKLVSILGGQPSVEAQSTGIR TALQMDDEKAEVKHYVTOAKDMGGMGGTAKVUTLTDNDNPKEFQKMS VDTERAKSYLKTEAKWHITKEFLISNGPKDTYVTKSYEDADEPPLAISYIHEV QENRAAGTVGRHAKODAANSQAPRYSDRHTLDREFTINPDEGEKTKTRPLDFF TAWMINITYFAEELHRIOQAOAQPYBLVNDNPAKATVQICSDOKPSNO PWTISADDKDPANGRPTISLPELIHNFENPVNDNNTAGYARRGGSRSRQD LYLFIVASDGJPPMESTNTLTKCGDVNGAHLSCHEAAYLNGLSGTALLL ACVILLVIVVKTVERQKIEPLIFEEVDYRQDIDTDDGEGEDTEADLTLQ RPSQINGITPRKDIKPYQOMPRGPURPAPNSVDDFTNTRQEAENDPAPPDSL QIYEGEGSVAGSLSLSESITSDDLDYLQWMPREKKLADLYSKDTPDDDS"	DEFINITION	DB 6; Length 2625;		BASE COUNT	15100 c	
BASE COUNT	730 a	559 t		ORIGIN	155100	
ORIGIN	661 c	575 g		Query Match	100.0%	
Query Match	100.0%	Score 18; DB 6; Length 2625;		Best Local Similarity	100.0%	
Best Local Similarity	100.0%	Pred. No. 41; Matches 18; Conservative 18; Mismatches 0; Indels 0; Gaps 0;		DEFINITION	Sequence 57 from patent US 5646250.	
DEFINITION	Sequence 57 from patent US 5646250.	DNA		ACCESSION	155100	
ACCESSION	155100.1	PAT 06-FEB-1997		VERSION	155100.1	
VERSION	G1:2476303	PAT 07-OCT-1997		KEYWORDS	Unknown.	
KEYWORDS	Unclassified.	I. (bases 1 to 2625)		SOURCE	Unknown.	
SOURCE	ORGANISM	Unclassified.		REFERENCE	1 (bases 1 to 2625)	
Db	185 GGC GGCTTGAACTGA 168	Suzuki,S.		AUTHORS	Suzuki,S.	
RBSLT 3	134433.c	GCG GCG CTGAACTGA 18		TITLE	Cadherin polypeptides	
LOCUS	134433	DNA		JOURNAL	Patent: US 5666250-A 57 08-JUL-1997;	
DEFINITION	Sequence 57 from patent US 5597725.	linear		FEATURES	Location/Qualifiers	
ACCESSION	134433	PAT 06-FEB-1997		SOURCE	I. .2625	
BASE COUNT	730 a	<i>/organism="unknown"</i>		BASE COUNT	730 a	
ORIGIN	661 c	675 g		ORIGIN	661 c	
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Best Local Similarity	100.0%	Pred. No. 41; Matches 18; Conservative 18; Mismatches 0; Indels 0; Gaps 0;		Best Local Similarity	100.0%	
DEFINITION	Sequence 57 from patent US 5597725.	DNA		DEFINITION	Sequence 57 from patent US 5646250.	
ACCESSION	134433	PAT 06-FEB-1997		ACCESSION	155100	

Query Match	100.0%	Score 18;	DB 6;	Length 2625;	
Best Local Similarity	100.0%	Pred. No. 41;	Mismatches 0;	Indels 0;	Gaps 0;
Matches	18;	Conservative			
Qy	1	GGCGCTTGAAACGTA	18		
Db	185	GGCGCTTGAAACGTA	168		
RESULT 6					
HOMCALLA/C					
LOCUS	HOMCALLA	2625 bp	mRNA	linear	PRI 29-JUN-1994
DEFINITION	Homo sapiens cadherin-11 mRNA, complete cds.				
ACCESSION	L34056				
VERSION	L34056.1				
KEYWORDS					
SOURCE	Homo sapiens fetus brain cDNA to mRNA.				
ORGANISM	Homo sapiens				
REFERENCE					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Diversity of the cadherin family: evidence for eight new cadherins in nervous tissue				
JOURNAL	Cell. Revolv. 2 (4), 261-270 (1991)				
MEDLINE	91283540				
PUBMED	2029658				
REFERENCE					
AUTHORS	Tanahara,H., Sano,K., Heimark,R.L., St.John,T. and Suzuki,S.				
TITLE	Cloning of five cadherins clarifies characteristic features of cadherin extracellular domain and provides further evidence for two structurally different types of cadherin				
JOURNAL	Cell Adhesion Commun. 2, 15-26 (1994)				
FEATURES					
source	1. (bases 1 to 2625) /organism="Homo sapiens" /db_xref="taxon:9606" /tissue_type="brain" /dev_stage="fetus" 155..2546 /function="cell adhesion" /note="putative" /citation=[1] /codon_start=1 /product="cadherin-11" /protein_id="PAAJ35622.1" /db_xref="GI:506404" /translation="MKENYCQALVCLGMCHSHAFDERRGLRPSFHHEKGKEGVQRSRGWNNQFVTEETGPVPPVGLRHDIDGDGNKYTLSEGAGTIVKIDSGNTHATKLDRERAYTITMAQVDRNTTNPLEPSEFVKVDINDPPELHEYHANPERSVNGSVIQTASDADPVGNSAKLVISLRQPTFSEAOIGIRTAIPNDMREAKERHVYHQVHGGTAVTITDVNDPKEPQLYQMSVSEAVPGEEVERVAKDPIDGENGLYVNDGMEFEITDYEGQVKKLKPVDPTTERAVSLVKEAVANHWDPKFLISNGKDTYVQEDPMLAISIHEVQENAAAGTVGRHAKODDAANSPIRSLDHTDRAFTNPEDGFKTRPLDREQTAMNITYFAEELHNHQAEQVPAVRLVQDNWAKPFAQPSFCSDQPKLSNOPTVITSAKKDDKAAPNPFITSPUPSIHPNFTWDNDTNTAGVYARRGGSSRQKOLYLPIVISDGCPMSNTLTIVCGDONGALLSCNAEVNLKAGLSTGAILACTIVLIVVWVFLRQKPLPVDFDNTRCQDADNPTRAPPYQSYQIYGEGRGSVAGSLSLSESATTDSDLDYDLYQWNPREFKLLADLGSKDTFDDDS"QIYGYERGSVAGSLSLSESATTDSDLDYDLYQWNPREFKLLADLGSKDTFDDDS"				
CDS					
FEATURES					
source	Clone distribution: MGC clone distribution information can be found through the T.M.A.G. E. Consortium/LINTL at: http://image.lnl.gov Series: IRAK Plate: 12 Row: 1 Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 575577. Location/Qualifiers				
CDS	1..340 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC-17193 IMAGE:4183901" /tissue_type="Brain, glioblastoma with EGFR amplification" /clone.lib="NCICGAP_Brn64" /lab.host="DH10B" /note="vector: pCMV-SPORT6" 175..2365 /codon.start=1 /product="Unknown (protein for MGC:17193)" /protein_id="PAAJ3609.1" /db_xref="GI:514088667" /translation="MKENYCQALVCLGMCHSHAFDERRGLRPSFHHEKGKEGVQRSRGWNNQFVTEETGPVPPVGLRHDIDGDGNKYTLSEGAGTIVIDDSGNTTHATKLDRERAYTITMAQVDRNTTNPLEPSEFVKVDINDPPELHEYHANPERSVNGSVIQTASDADPVGNSAKLVISLRQPTFSEAOIGIRTAIPNDMREAKERHVYHQVHGGTAVTITDVNDPKEPQLYQMSVSEAVPGEEVERVAKDPIDGENGLYVNDGMEFEITDYEGQVKKLKPVDPTTERAVSLVKEAVANHWDPKFLISNGKDTYVQEDPMLAISIHEVQENAAAGTVGRHAKODDAANSPIRSLDHTDRAFTNPEDGFKTRPLDREQTAMNITYFAEELHNHQAEQVPAVRLVQDNWAKPFAQPSFCSDQPKLSNOPTVITSAKKDDKAAPNPFITSPUPSIHPNFTWDNDTNTAGVYARRGGSSRQKOLYLPIVISDGCPMSNTLTIVCGDONGALLSCNAEVNLKAGLSTGAILACTIVLIVVWVFLRQKPLPVDFDNTRCQDADNPTRAPPYQSYQIYGEGRGSVAGSLSLSESATTDSDLDYDLYQWNPREFKLLADLGSKDTFDDDS"QIYGYERGSVAGSLSLSESATTDSDLDYDLYQWNPREFKLLADLGSKDTFDDDS"				
BASE COUNT	730 a 661 c 675 g 559 t				
ORIGIN					
Query Match	100.0%	Score 18;	DB 9;	Length 2625;	
Best Local Similarity	100.0%	Pred. No. 41;	Mismatches 0;	Indels 0;	Gaps 0;
Matches	18;	Conservative			
Qy	1	GGCGCTTGAAACGTA	18		
Db	185	GGCGCTTGAAACGTA	168		
RESULT 7					
BC013609/c					
LOCUS	BC013609	3440 bp	mRNA	linear	PRI 07-SEP-2001
DEFINITION	Homo sapiens, clone MGC:17193 IMAGE:4183901, mRNA, complete cds.				
ACCESSION	BC013609				
VERSION	BC013609.1				
KEYWORDS	MGC.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 3440)				
TITLE	Direct Submission				
JOURNAL	Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2599, USA				
COMMENT	NIH MGC Project URL: http://mgc.nci.nih.gov				
REMARK	Contact: MGC help desk Email: cgapps-r@mail.nih.gov				
CDNA	Tissue Procurement: David N. Louis, M.D. CDNA Library Preparation: Life Technologies, Inc.				
LIBRARY	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)				
DNA	Sequencing by: Baylor College of Medicine Human Genome Sequencing Center				
SEQUENCING	Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: viallon@bcm.tmc.edu				
CONTACT	Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.				
Sequencing	Sequencing Center code: BCM-HGSC				
Center	Clone code: MGC				
clone	Clone distribution: MGC clone distribution information can be found through the T.M.A.G. E. Consortium/LINTL at: http://image.lnl.gov				
clone	Series: IRAK Plate: 12 Row: 1 Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 575577.				
clone	Location/Qualifiers				
clone	1..340 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC-17193 IMAGE:4183901" /tissue_type="Brain, glioblastoma with EGFR amplification" /clone.lib="NCICGAP_Brn64" /lab.host="DH10B" /note="vector: pCMV-SPORT6" 175..2365 /codon.start=1 /product="Unknown (protein for MGC:17193)" /protein_id="PAAJ3609.1" /db_xref="GI:514088667" /translation="MKENYCQALVCLGMCHSHAFDERRGLRPSFHHEKGKEGVQRSRGWNNQFVTEETGPVPPVGLRHDIDGDGNKYTLSEGAGTIVIDDSGNTTHATKLDRERAYTITMAQVDRNTTNPLEPSEFVKVDINDPPELHEYHANPERSVNGSVIQTASDADPVGNSAKLVISLRQPTFSEAOIGIRTAIPNDMREAKERHVYHQVHGGTAVTITDVNDPKEPQLYQMSVSEAVPGEEVERVAKDPIDGENGLYVNDGMEFEITDYEGQVKKLKPVDPTTERAVSLVKEAVANHWDPKFLISNGKDTYVQEDPMLAISIHEVQENAAAGTVGRHAKODDAANSPIRSLDHTDRAFTNPEDGFKTRPLDREQTAMNITYFAEELHNHQAEQVPAVRLVQDNWAKPFAQPSFCSDQPKLSNOPTVITSAKKDDKAAPNPFITSPUPSIHPNFTWDNDTNTAGVYARRGGSSRQKOLYLPIVISDGCPMSNTLTIVCGDONGALLSCNAEVNLKAGLSTGAILACTIVLIVVWVFLRQKPLPVDFDNTRCQDADNPTRAPPYQSYQIYGEGRGSVAGSLSLSESATTDSDLDYDLYQWNPREFKLLADLGSKDTFDDDS"QIYGYERGSVAGSLSLSESATTDSDLDYDLYQWNPREFKLLADLGSKDTFDDDS"				
BASE COUNT	1055 a 774 c 792 g 819 t				
ORIGIN					
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Best Local Similarity	100.0%	Pred. No. 38;	Mismatches 0;	Indels 0;	Gaps 0;
Matches	18;	Conservative			
Qy	1	GGCGCTTGAAACGTA	18		
Db	185	GGCGCTTGAAACGTA	168		

ORIGIN

RESULT 11		RESULT 12	
QRY	DB	REFERENCE	REFERENCE
HUMOSF4B/C	HUMOSF4B	Query Match Best Local Similarity 100.0%; Score 18; DB 6; Length 3712; Matches 18; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;	Query Match Best Local Similarity 100.0%; Score 18; DB 5; Length 3914; Matches 18; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;
		DEFINITION Human mRNA for OB-cadherin-2, complete cds.	DEFINITION Sequence 5 from Patent US 5869638.
		ACCESSION D21255	ACCESSION AR034823
		VERSION D21255.1	VERSION AR034823.1
		KEYWORDS osf-4; OB-cadherin-2.	KEYWORDS
		SOURCE Homo sapiens	SOURCE Unknown.
		ORGANISM Homo sapiens	ORGANISM Unknown.
REFERENCE		1 (sites)	Unclassified.
AUTHORS		Okazaki,M., Takeshita,S., Kawai,S., Kikuno,R., Tsujimura,A.,	I (bases 1 to 3914)
TITLE		Molecular cloning and characterization of OB-cadherin, a new member of cadherin family expressed in osteoblasts	Takeshita,S., Okazaki,M., Kawai,S., and Amann,E.
JOURNAL		J. Biol. Chem. 269 (16), 12091-12098 (1994)	JOURNAL Bone-related cadherin-like protein and process for its production
MEDLINE		94216322	Patent: US 5869638-A 5 09 FEB 1999;
REFERENCE		2 (bases 1 to 3867)	Location/Qualifiers
AUTHORS		Kikuno,R.	1. .3914
TITLE		Direct Submission	source
JOURNAL		Submitted (21-Oct-1993) Reiko Kikuno, Hoechst Japan Ltd., Pharma Research Lab., 1-3-2 Minami-dai, Kawagoe, Saitama 350-11, Japan (E-mail:r.kikuno@dbj.hg.ac.jp, Tel:0492-43-6149, Fax:0492-43-2479)	BASE COUNT 1110 a /organism="unknown"
FEATURES	source	1. .3867 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="PK0161" /issue_type="Osteosarcoma" /stage="new born"	DB 502 GCGGCTTGAAACAGTA 503
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CDS		DEFINITION cDNA encoding human OSF-4.	DEFINITION
		ACCESSION E07383	ACCESSION
		VERSION E07383.1	VERSION
		KEYWORDS	JP 1994122700-A/3.
		ORGANISM Homo sapiens	ORGANISM
REFERENCE		Bukuryo; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens	Bukuryo; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens
AUTHORS		1 (bases 1 to 3914)	1 (bases 1 to 3914)
TITLE		Takeshita,A., Okazaki,M., Kawai,S., Tsujimura,A. and Aman,E.	PI 1993112883
JOURNAL		PATENT: JP 1994122700-A 3 06-MAY-1994;	PI 1993112883
COMMENT		HOECHST JAPAN LTD	HOECHST JAPAN LTD
OS		Homo sapiens (human)	Homo sapiens (human)
PN		JP 1994122700-A/3	JP 1994122700-A/3
PD		06-MAY-1994	06-MAY-1994
PR		13-JUL-1994	13-JUL-1994
PR		JP 1993112883	JP 1993112883
PR		28-AUG-1992	28-AUG-1992
PR		JP 92P 230038	JP 92P 230038
PI		TAKESHITA, ATUSHI; OKAZAKI, MAKOTO; KAWAI, SHINJI; PI	TAKESHITA, ATUSHI; OKAZAKI, MAKOTO; KAWAI, SHINJI; PI
PI		TSUTUMA, AMANO; EGON	TSUTUMA, AMANO; EGON
PI		C07K13/00, A61K37/02, A61K37/02, A61K39/395, A61K39/395, A61K49/00,	C07K13/00, A61K37/02, A61K37/02, A61K39/395, A61K39/395, A61K49/00,
PI		C07K15/14, C12P21/02, C12P21/02;	C07K15/14, C12P21/02, C12P21/02;
CC		strandedness: Double;	strandedness: Double;
CC		topology: Linear;	topology: Linear;
CC		hypothetical: No;	hypothetical: No;
CC		anti-sense: No;	anti-sense: No;
KEY		Location/Qualifiers	Location/Qualifiers
FH		source 1. .3914	source 1. .3914
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FT		/cell-type="primary bone cancer"	/cell-type="primary bone cancer"
FT		/clone="PK0161"	/clone="PK0161"
FT		5'-UTR	5'-UTR
CDS		1. .490	1. .490
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FT		/product="Human OSF-4"	/product="Human OSF-4"
FEATURES		Location/Qualifiers	Location/Qualifiers

source	ACCESSION	AC0068656
BASE COUNT	VERSION	AC06856.2
ORIGIN	KEYWORD	GI:9295747
Query Match	organism="Homo sapiens"	/ab_xref=taxon:9606*
LOCUS	SOURCE	/ab_xref=taxon:9606 t
Best local Similarity	ORGANISM	Homo sapiens
Matches	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
18; Conservative	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
0; Mismatches	TITLE	I (bases 1 to 18994)
0; Indels	JOURNAL	DOE Joint Genome Institute.
0; Gaps	REFERENCE	Sequencing of Human Chromosome 16
Db	AUTHORS	2 (bases 1 to 18994)
	TITLE	DOE Joint Genome Institute.
	JOURNAL	Submitted (06-MAY-2000) Production Sequencing Facility, DOE Joint
		Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
		On Jul 20, 2000 this sequence version replaced 91:7712105.
	COMMENT	-----
		Genome Center
		Center Code: JGI
		Web site: http://www.jgi.doe.gov
SOURCE	Project Information	
ORGANISM	Center Project Name: 1258011	
Homo sapiens	Center clone name: C1T978SKA_186A5	
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	Summary Statistics	
AUTHORS	Consensus quality: 17227 bases at least Q30	
DOI	Consensus quality: 185750 bases at least Q30	
Joint Genome Institute and Stanford Human Genome Center.	Consensus quality: 187169 bases at least Q20	
TITLE	Estimated insert size: 171860; agarose-fp estimation	
JOURNAL	Estimated insert size: 18884; sun-of-contigs estimation	
REFERENCE	Quality coverage: 7.12 in 020 bases; agarose-fp estimation	
AUTHORS	Quality coverage: 6.48 in 020 bases; sum-of-contigs estimation.	
DOI	* NOTE: This is a working draft sequence. It currently	
Joint Genome Institute and Stanford Human Genome Center.	* consists of 22 contigs. Gaps between the contigs	
TITLE	* are represented as runs of N. The order of the pieces	
JOURNAL	* is believed to be correct as given, however the sizes	
Submitted (28 NOV-2000) DOE Joint Genome Institute, 2800 Mitchell	* of the gaps between them are based on estimates that have	
Drive, Walnut Creek, CA 94598, USA	* provided by the submitter.	
COMMENT	* this sequence will be replaced	
	* by the finished sequence as soon as it is available and	
	* the accession number will be preserved.	
	WI-9802 603521	*
FEATURES	1. 153588	*
SOURCE	Location/Qualifiers	*
	1. /clone="RP11-22903"	*
	/organism="Homo sapiens"	*
	/ab_xref=taxon:9606*	*
	/chromosome="16"	*
BASE COUNT	/clone="RP11-22903"	*
ORIGIN	a 29627 c 29013 g 46234 t	*
Query Match	100.0%; Score 18; DB 9; Length 153588;	*
Best local Similarity	100.0%; Pred. No. 12; Length 153588;	*
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	*
Qy	1 GGCGCTGTAAACAGTA 1B	*
Db	133378 GGCGCTGTAAACAGTA 1B3395	*
RESULT	15	*
AC008656	AC058656	189894 bp DNA linear HTG 20-JUL-2000
DEFINITION	Homo sapiens chromosome 16 clone CTA-186A5, WORKING DRAFT SEQUENCE,	22 ordered pieces.

```

*      95032   95951: contig of 920 bp in length
*      95952   96051: gap of unknown length
*      96052   138399: contig of 42347 bp in length
*      138399   138438: gap of unknown length
*      138438   138499: contig of 5470 bp in length
*      138499   143988: gap of unknown length
*      143988   144069: contig of 8700 bp in length
*      144069   152768: gap of unknown length
*      152769   152869: contig of 974 bp in length
*      152869   153842: gap of unknown length
*      153842   153943: contig of 12695 bp in length
*      153943   166639: gap of unknown length
*      166639   166739: contig of 23156 bp in length.
*      166739 Location.Qualifiers
*      1. 189894
*          /organism="Homo sapiens"
*          /db_xref="taxon:9606"
*          /chromosome="16"
*          /clone="CITA-186A5"
*          /clone_id="54101"
*          human BAC library A"
*          54101 t 2106 Others
*          37380 c 36768 g
*          59539 a
*          RIGIN
*          USE COUNT

```

```

Query Match      100.0%; Score 18; DB 2; Length 189894;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GGGGGCTTGTAACAGTA 18
Db      81209 GGCGGCCTTGTAACAGTA 81226

```

Search completed: June 22, 2003, 08:44:00
 Job time : 1921 secs

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—

increasingly different cancer types. The following table summarizes the results of our study.

standard,
0 (first
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0.
9; 99%
8; 98%
IV BRITI-
CD:
36555687/
or dec-
ation or
ers -

pression
nucleotides
differences
size; ss
alignments

n or fun
tide OB-1
ntiation

carcinogenesis, 1990, 10, 101-106. © 1990 Blackwell Science Ltd

XX
 PS Claim 11; Page 22; 37pp; English.
 XX
 CC The present sequence is an antisense oligonucleotide for the human
 CC cadherin-11 (cad-11) mRNA. It can be used to reduce the levels of cad-11
 CC expression in cells, which is useful in the treatment of carcinomas,
 CC particularly prostate tumour cells, for modulating the differentiation
 CC of cells, and in the prevention or termination of pregnancy. It is
 XX particularly useful for preventing metastasis of tumour cells.
 SO Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 other;
 Query Match 100.0%; Score 18; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0;
 Matches 18; Conservative 0; Indels 0; Gaps 0;
 QY 1 GCGGGCTTGAAACGTA 18
 DR 1 GCGGGCTTGAAACGTA 18
 DB 1 GCGGGCTTGAAACGTA 18
 RESULT 2
 ID AAT85403/C
 XX AAT85403 standard; cDNA; 2625 BP.
 AC AAT85403;
 XX 03-NOV-1997 (first entry)
 DE Human cadherin-11 coding sequence.
 XX Human; cadherin; rat; calcium-dependent cell adhesion protein;
 KW superfamily; cytoskeleton; eatenin; cancer; ss.
 XX Homo sapiens.
 OS
 PH KEY Location/Qualifiers
 FT CDS 156..2546
 FT /*tag= a
 FT /product= Cadherin-11
 XX US5646250-A.
 PD 08-JUL-1997.
 XX 17-APR-1992; 92US-0872643.
 PR 19-APR-1993; 93US-0049460.
 PR 17-APR-1992; 92US-0872643.
 PR 01-NOV-1994; 94US-0332638.
 PR (DOHE-) DOHENY EYE INST.
 PA XX
 PI Suzuki S;
 PT XX
 DR WPI; 1997-362997/33.
 XX
 PR Human and rat cadherin polypeptide(s) - mediate cell-cell adhesion
 PS Example 2; Column 87-90; 56pp; English.
 XX
 CC This sequence encodes human cadherin-11. The invention specifically
 CC provides details of human cadherin-5, -8, -11, -12 and -13, and rat
 CC cadherin-8,-5,-11 and -13. Cadherins are calcium-dependent cell
 CC adhesion proteins. They are glycosylated integral membrane proteins
 CC that have an N-terminal extracellular domain that determines binding
 CC specificity, a hydrophobic membrane spanning region and a C-terminal
 CC cytoplasmic domain, which is highly conserved among members of the
 CC superfamily. The C-terminal domain interacts with the cytoskeleton
 CC through eatenins and other cytoskeleton-associated proteins. The
 CC cadherin proteins may be used in the analysis of the role of
 CC proteins also allows investigation of the structure and function of
 XX
 CC cadherin. The cadherin proteins may be isolated by using anti-cadherin
 CC antibodies. These antibodies may also be used to modulate the activity
 CC of cadherin and to determine the tissue specific distribution of cadherin
 CC proteins. Each subclass of cadherins has a unique tissue distribution
 CC pattern.
 XX Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;
 Query Match 100.0%; Score 18; DB 18; Length 2625;
 Best Local Similarity 100.0%; Pred. No. 3; 3.4; Mismatches 0;
 Matches 18; Conservative 0; Indels 0; Gaps 0;
 QY 1 GCGGGCTTGAAACGTA 18
 DR 1 GCGGGCTTGAAACGTA 18
 DB 185 GCGGGCTTGAAACGTA 186
 RESULT 3
 ID AAT61925/C
 XX AAT61925 standard; cDNA; 2625 BP.
 AC AAT61925;
 XX 14-MAY-1997 (first entry)
 DE Full length human cadherin-11 cDNA.
 XX
 KW Ca2+ dependent; cell adhesion protein; foetal; cadherin; rat;
 KW brain; human; antibody; purification; determination; calcium ion; ss.
 KW tissue expression; binding antagonist; calcium ion; ss.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 156..2546
 FT /*tag= a
 FT /product= Cadherin-11
 XX US5597725-A.
 XX
 PD 28-JAN-1997.
 XX
 PR 17-APR-1992; 92US-0872643.
 PR 26-JAN-1994; 94US-0188228.
 PR 19-APR-1992; 92US-0872643.
 PR 19-APR-1993; 93US-0049460.
 PR (DOHE-) DOHENY EYE INST.
 PA XX
 PI Suzuki S;
 PT XX
 DR WPI; 1997-108328/10.
 XX
 DR P-PSDB; AAW13134.
 XX
 PT Antibodies to cadherin proteins - useful as cadherin antagonists,
 PT etc.
 XX
 PS Example 2; Columns 91-96; 59pp; English.
 XX
 CC The present sequence encodes full length human cadherin-11, which
 CC is a Ca2+ dependent cell adhesion protein. The human cadherin cDNA
 CC was isolated from a foetal brain cDNA library, using probes based
 CC on homologous rat cadherin cDNA.
 CC Antibodies or fragments that specifically bind the human cadherin
 CC can be used to purify the cadherin, determine its tissue expression
 CC and antagonise its ligand/antiligand binding activities.
 XX Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;
 Query Match 100.0%; Score 18; DB 18; Length 2625;
 Best Local Similarity 100.0%; Pred. No. 3; 3.4; Mismatches 0;
 Matches 18; Conservative 0; Indels 0; Gaps 0;

QY 1 GCGGCCTGTTAACAGTA 18
 ||||||| 168

Db 185 GCGGCCTGTTAACAGTA 168

RESULT 4

AY83124/C
 ID AAV83124 standard; cDNA; 2625 BP.

XX AAV83124;

XX 02-MAR-1999 (first entry)

DE Cadherin-11 cDNA.

XX Cadherin; morphogenesis; calcium-dependent cell adhesion; pregnancy; XX KW endometrium; trophoblast; blastocyst; infertility; ss.

OS Homo sapiens.

VX

Key CDS Location/Qualifiers

FT 155..2545 /itag= a /product= Cadherin-11

FT XX W09849560-A1.

PN XX 05-NOV-1998.

PD XX 24-APR-1998; 98WO-CA00397.

PF XX 25-APR-1997; 97CA-2203718.

PR XX (UYBR-) UNIV BRITISH COLUMBIA.

PA XX Maccallum CD, Stephenson MD;

PT XX WPI; 1999-024071/02.

DR XX P-PSDB; AAW85598.

XX

PT Assessing likelihood of successful pregnancy by measuring levels of PT coherin-11 in endometrium - also diagnosis of infertility from low PT progestin or cadherin-encoding DNA

XX

PS Claim 7; Page 52-53; 63PP; English.

XX

The likelihood of establishing and maintaining a pregnancy, blastocyst implantation or endometrial receptivity are determined by measuring the level of cadherin-11 mRNA or protein in endometrial cells. A level below a standard value indicates inability to establish or maintain pregnancy. Women who are identified as having low level expression of cadherin-11 in endometrial cells can then be treated with a genetic construct comprising the cadherin-11 cDNA. The expression of cadherin-11 from the construct increases fertility and lessens the likelihood of miscarriage.

CC Cadherin-11 expression is a better predictor of endometrial response and receptiveness than conventional analysis of endometrial cell morphology.

XX Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 2625;
 Best Local Similarity 100.0%; Pred. No. 3,4; Mismatches 0; Indels 0; Gaps 0;

SQ 1 GCGGCCTGTTAACAGTA 18
 ||||||| 168

Db 185 GCGGCCTGTTAACAGTA 168

RESULT 5

AAE55586 standard; DNA; 2625 BP.

ID AAE55586;

XX DT 29-MAY-2001 (first entry)

XX DE Nucleotide sequence of a human cadherin-11 polypeptide.

XX Human; cadherin-11; inflammatory joint disorder; chronic synovitis; XX KW autoimmune disorder; rheumatoid arthritis; arthritis; ss.

OS Homo sapiens.

VX

Key CDS Location/Qualifiers

FT 156..2545 /itag= a /product= "cadherin-11"

FT XX WO200117557-A1.

PN XX 15-MAR-2001.

PD XX 01-SEP-2000; 2000WO-US24101.

PF XX 03-SEP-1999; 99US-0152456.

PR XX 13-SEP-1999; 99US-0153490.

PA XX (IGHM) BRIGHAM & WOMENS HOSPITAL INC.

XX Brenner MB, Valencia X;

PT XX WPI; 2001-235163/24.

DR XX P-PSDB; AAB67624.

XX

PT Treating inflammatory joint disorders, e.g. chronic synovitis, PT autoimmune disorders and rheumatoid arthritis, comprises administering PT a cadherin-11 inhibitor that inhibits the binding of cadherin-11 to its counter receptor.

XX

PS Disclosure; Page 78-82; 89PP; English.

XX

The present sequence encodes a human cadherin-11 polypeptide. Cadherin-11 is a transmembrane molecule that, inter alia, mediates CC binding of cells to each other through interaction with itself or its CC counter-receptors. Agents which inhibit cadherin-11, or which inhibit CC the binding of cadherin-11 to a cadherin-11 counter receptor are used CC to treat a subject having an inflammatory joint disorder. The method is useful for treating inflammatory joint disorders, e.g. chronic synovitis, CC autoimmune disorders, rheumatoid arthritis, lyme disease arthritis, CC arthritis associated with inflammatory bowel disease or with ankylosing CC spondylitis, Reiter's syndrome, or arthritis associated with systemic CC lupus erythematosus. The method may also be used for the rational drug design of new agents capable of modulating an immune system response. CC The nucleotide and amino acid sequences of cadherin-11 modulating agents CC may be used in computer-based modelling systems to predict the secondary CC and tertiary structure of the extracellular domain, and to target a toxin or a detectable agent to cells which express cadherin-11 CC counter-receptors or cadherin-11. The antibodies inhibiting the binding CC of cadherin-11 to its counter receptor may be used in screening assays CC for identifying pharmaceutical lead compounds in molecular libraries.

SQ Sequence 2625 BP; 730 A; 661 C; 675 G; 559 T; 0 other;

Query Match 100.0%; Score 18; DB 22; Length 2625;
 Best Local Similarity 100.0%; Pred. No. 3,4; Mismatches 0; Indels 0; Gaps 0;

Db 185 GCGGCCTGTTAACAGTA 168

RESULT 6

AAQ4392/C
 ID AAQ4392 standard; cDNA to mRNA; 3712 BP.
 XX
 AC AAQ4392;
 XX
 DT 14-SEP-1994 (first entry)
 XX
 DE Sequence of human OSF-4-1 cDNA.
 XX
 KW OSF-4-1; cadherin; growth factor; osteogenesis; osteoblast; therapy;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT CDS 461..2851 /*tag= a
 XX EP595801-A.
 PN 09-MAR-1994.
 XX PR 25-AUG-1993; 93EP-0113602.
 XX PR 28-AUG-1992; 92JP-0230028.
 PA (FARR) HOECHST JAPAN LTD.
 XX PT Amann, E., Kawai, S., Okazaki, M., Takeshita, S., Tsujimura, A.;
 DR WPI; 1994-076152/10.
 DR P-PSDB; AAR49731.
 XX
 New bone related, cadherin-like OSF-4 proteins - for treatment and diagnosis of bone metabolic disease, and nucleic acid encoding them
 XX Claim 3; Page 18-22; 34PP; English.
 CC cDNA libraries were constructed from the mouse osteoblastic cell line MC3T3-El and from mouse liver tissue, amplified by PCR, and then as much common DNA as possible removed by hybridisation between the 2 libraries. Residual El-specific DNA was amplified, inserted into lambda gt10 and screened by plaque hybridisation. A minibank of 273 El-specific clones was recovered, their inserts amplified and used to screen total RNA from both cell types. One clone specific for El was identified and sequenced. The insert from this clone was used to screen cDNA prep. from El RNA and the longest pos. insert cloned in pGEM 11ZF (+) to give PK0164. This insert was sequenced; it encoded the 796 AA mouse precursor protein (AAQ44391/R49730). The osteosarcoma to identify 2 clones encoding the 2 human precursor proteins - OSF-4-1 and OSF-4-2 (AAQ4392/R49731 and AAQ44393/R49732
 XX Sequence 3712 BP; 1074 A; 856 C; 897 G; 885 T; 0 other;
 CC Query Match 100.0%; Score 18; DB 15; Length 3712;
 CC Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Sequence 3867 BP; 1098 A; 905 C; 932 G; 932 T; 0 other;
 CC Query Match 100.0%; Score 18; DB 24; Length 3867;
 CC Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 SQ Sequence 3867 BP; 1098 A; 905 C; 932 G; 932 T; 0 other;
 CC Query Match 100.0%; Score 18; DB 24; Length 3867;
 CC Best Local Similarity 100.0%; Pred. No. 3.5; Mismatches 0; Indels 0; Gaps 0;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 RESULT 7
 ABK35485/C
 ID ABK35485 standard; DNA; 3867 BP.
 XX
 AC ABK35485;
 XX
 DT 08-MAY-2002 (first entry)

AAQ4392/C
 ID AAQ4392 standard; cDNA to mRNA; 3914 BP.
 XX
 AC AAQ4392;
 XX
 DT 14-SEP-1994 (first entry)
 XX
 DE Sequence of human OSF-4-2 cDNA.
 XX
 KW OSF-4-2; cadherin; growth factor; osteogenesis; osteoblast; therapy;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.

FH Location/Qualifiers
FT 491..2569
FT /*tag- a
PN XX
EP585801-A.
XX
XX PD 09-MAR-1994.
XX
PF 25-AUG-1993; 93EP-0113602.
XX PR 28-AUG-1992; 92JP-023002B.
XX PA (FARH) HOECHST JAPAN LTD.
XX PI Amann, E., Kawai, S., Okazaki, M., Takeshita, S., Tsujimura, A.;
XX DR WPI; 1994-076152/10.
DR P-PSDB; AAR4932.
XX P-PSDB; AAB59534.
XX DR WPI; 2001-112393/12.
DR P-PSDB; AAB59534.
XX PT Identifying prion protein binding proteins for use in diagnosis, treatment or prion-related diseases, neurodegenerative disorders, by detecting complex formation with detectable prion protein fusion protein -
PT Disclosure; Page -; 77pp; English.
PS
XX Claim 3; Page 23-27; 34pp; English.
XX cDNA libraries were constructed from the mouse osteoblastic cell line MC3T3-El and from mouse liver tissue, amplified by PCR, and then as much common DNA was possible removed by hybridisation between the 2 libraries. Residual El-specific DNA was amplified, inserted into lambda gt10 and screened by plaque hybridisation. A minibank of 273 E-specific clones was recovered, their inserts amplified and used to screen total RNA from both cell types. One clone specific for El was identified and sequenced. The insert from this clone was used to screen cDNA prep. from El RNA and the longest posn. insert cloned in pGEM 1Zf (+) to give pR0164. This insert was sequenced; it encoded the 796 AA mouse precursor protein (AAQ4391/R49730). The insert was also used to screen a cDNA bank prep. from human osteosarcoma to identify 2 clones encoding the 2 human precursor proteins - OSF-4-1 and OSF-4-2 (AAQ4392/R49731 and AAQ4393/R49732 respectively).
XX Sequence 3914 BP; 1105 A; 920 C; 947 G; 942 T; 0 other;
Query Match 100.0%; Score 18; DB 15; Length 3914;
Best Local Similarity 100.0%; Pred. No. 3 5; Mismatches 0; Indels 0; Gaps 0;
XX OY 1 GCGGGTTAACAGTA 18
||||| 520 GCGGGCTGTAAACAGTA 503
RESULT 9
AAF5934/C
ID AAF5934 standard; cDNA; 3489 BP.
XX
AC AAF5934;
XX DT 24-APR-2001 (first entry)
XX DE cDNA encoding a mouse PrP-binding protein, OB-cadherin-1.
XX
KW Mouse OB-cadherin-1; murine; prion protein binding protein; PrPBP;
KW detectable PrP fusion protein; detection; diagnosis; B lymphocyte;
KW PrP-Sc-associated disorder; prion disease; Creutzfeldt-Jakob disease;
KW CID; Kuru; fatal familial insomnia; scrapie; BSE;
KW bovine spongiform encephalopathy; PrP-C-associated disorder;
KW cancer; neurodegenerative disorder; immunological disorder;
KW abnormal immunoglobulin secretion; lymphoma; multiple myeloma;
KW monoclonal gammopathy; B cell related autoimmune disease;
KW myasthenia gravis; rheumatoid arthritis; ss.
XX OS Mus musculus.

XX WO200100235-A1.
PN 04-JAN-2001.
XX PD 29-JUN-2000; 2000WO-US17927.
XX PR 29-JUN-1999; 99US 0342426.
PA (UWMC-) UNIV MCGILL.
PA (CAPR-) CARRION PHARM INC.
XX PI Cashman NR, Dodelet V, Paramithiotis E;
XX DR WPI; 2001-112393/12.
DR P-PSDB; AAB59534.
XX PT Identifying prion protein binding proteins for use in diagnosis, treatment or prion-related diseases, neurodegenerative disorders, by detecting complex formation with detectable prion protein fusion protein -
PT Disclosure; Page -; 77pp; English.
XX The invention relates to a method of identifying a prion protein binding protein (PrPBP). The method comprises contacting a cell or biological sample with a detectable prion protein (PrP) fusion protein under conditions that allow complex formation between the PrP and a PrPBP, and detecting the complex, enabling the PrPBP to be identified. The invention also relates to a method for identifying a nucleic acid molecule which encodes PrPBP, which comprises providing a population of cells expressing a pool of nucleic acid molecules, where the cells do not normally express PrP on their cell surfaces, exposing the population of cells to detectably labelled PrP, and identifying a cell which binds the detectably labelled PrP, thereby enabling the nucleic acid encoding the PrPBP to be identified. The invention further relates to a method of detecting the abnormally folded pathogenic PrP isoform (Pr-Sc) in a sample using a PrPBP identified according to the invention; a method for screening potential inhibitors of Pr-Sc/PrP binding; the use of a PrPBP or PrP-binding portion thereof to inhibit Pr-Sc activity in a mammal or biological sample; the use of a PrPBP or PrP-binding portion thereof to treat a disorder associated with an undesirable level of interaction between the normally folded PrP-C and PrP-B in a mammal; and a method of detecting B lymphocytes in a biological sample using a PrPBP. The invention also encompasses fusion proteins comprising prp fused to alkaline phosphatase, or a PrPBP fused to alkaline phosphatase. PrPps, or the PrP-binding portions thereof, are useful for treating a disorder associated with PrP. The disorder may be a PrP-Sc-related disorder such as Creutzfeldt-Jakob disease (CJD), kuru, fatal familial insomnia in humans, scrapie in sheep, and bovine spongiform encephalopathy (BSE) in cattle. The disorder may also be one associated with an undesirable level of interaction between the normally folded PrP-C and a PrPBP in a mammal such as cancer, neurodegenerative disorders, immunological disorders, abnormal proliferation or secretion of immunoglobulin, lymphoma, multiple myeloma, monoclonal gammopathy, B cell-related autoimmune diseases, myasthenia gravis, or rheumatoid arthritis. The present sequence represents cDNA encoding murine OB-cadherin-1 which was identified as a moderate affinity PrPBP in the invention.
CC Note: The present sequence is not shown in the specification, but CC was obtained from GenBank (accession number D21253).
XX Sequence 3489 BP; 1053 A; 763 C; 791 G; 882 T; 0 other;
Query Match 91.1%; Score 16.4%; DB 22; Length 3489;
Best Local Similarity 94.4%; Pred. No. 27; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCGGGCTGTAAACAGTA 18
||| 299 GGCAGCTGTAAACAGTA 282
DB

PT tissues useful for determining the presence of colon cancer in a cell
 PT or tissue type, and in antisense therapy -
 XX
 PS Claim 1; Fig 1; 796pp; English.

CC ABO56106 to ABO60787 represent isolated nucleic acids (I) differentially
 CC expressed in cancer tissues. ABB8993 to ABB7904 represent proteins
 CC encoded by the ABO60776 to ABO60787 nucleic acid sequences. (I) can be
 CC used in antisense therapy. An antibody immunoreactive with a polypeptide
 CC encoded by (I) is useful for detecting cancer in a patient sample, and
 CC for detecting the presence or absence of a polynucleotide encoded by a
 CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
 CC from (I) can be used for determining the presence of a nucleic acid which
 CC hybridises to (I), and for determining the phenotype of cells in a sample
 CC of cells from a patient. (I) is useful for determining the presence of
 CC colon cancer in a cell or tissue type, for determining the presence or
 CC state of other type of cancer, in antisense therapy, to generate
 CC macroarrays on a solid surface, to identify a chromosome on which the
 CC corresponding gene resides, and in tissue profiling, forensics, genetic
 CC analysis, mapping and diagnostic applications. (I) can be used to raise
 CC antibodies, and to screen for peptide analogues and antagonists.
 XX

SQ Sequence 654 BP; 199 A; 122 C; 158 G; 168 T; 7 other;

Query Match	85 6%	Score 15.4;	DB 24;	Length 654;
Best Local Similarity	94 1%	Pred. No. 83;	Mismatches 0;	
Matches	16;	Conservative		

Oy 1 GCGGGCTTGTAAACAGT 17
 Db 186 GCGGCGTTGTGACAGT 202

RESULT 15

ID AAH03710	Standard; cDNA; 808 BP.
XX	
AC AAH03710;	
XX	
DT 26-JUN-2001 (first entry)	
XX	
DE Human cDNA clone (5'-primer) SEQ ID NO:545.	
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.	
XX	
OS Homo sapiens.	
XX	
EP1074617-A2.	
CD 07-FEB-2001.	
XX	
PR 28-JUL-2000; 2000ER-0116126.	
XX	
PR 29-JUL-1999; 999P-0248036.	
PR 27-AUG-1999; 999P-0300253.	
PR 11-JAN-2000; 2000P-0118776.	
PR 02-MAY-2000; 2000P-0183767.	
PR 09-JUN-2000; 2000P-0241899.	
PA (HELI-) HELIX RES INST.	
XX	
PI ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;	
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;	
XX	
DR WPI; 2001-318749/34.	
XX	
PT Primer sets for synthesizing polynucleotides, particularly the 5602	
PT full-length cDNAs defined in the specification, and for the detection	
PT and/or diagnosis of the abnormality of the proteins encoded by the	
XX full-length cDNAs -	
PS Claim 1; SEQ ID 545; 2537pp + CD ROM; English.	
XX	

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dR primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH0166 to AAH1628 and AAH1363 to AAH18742 represent human cDNA sequences; AB92446 to AB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

SQ Sequence 808 BP; 265 A; 149 C; 200 G; 191 T; 3 other;

Query Match	85 6%	Score 15.4;	DB 22;	Length 808;
Best Local Similarity	94 1%	Pred. No. 85;	Mismatches 0;	
Matches	16;	Conservative		

Oy 1 GCGGGCTTGTAAACAGT 17
 Db 123 GCGGCGTTGTGACAGT 139

Search completed: June 22, 2003, 08:11:48
 Job time : 240 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:06:44 ; search time 49 Seconds
 (without alignments)
 112.657 million cell updates/sec

Title: US-09-830-811-1
 Perfect score: 18
 Sequence: 1 ggccggcttgtaaacacgtt 18

Scoring table: IDENTITY NUC
 Gapext 1.0
 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

Issued_Patents_NA.*

1: /cggn_6/pctdata/1/ina/5A_COMB.seq; *
 2: /cggn_6/pctdata/1/ina/5B_COMB.seq; *
 3: /cggn_6/pctdata/1/ina/6A_COMB.seq; *
 4: /cggn_6/pctdata/1/ina/6B_COMB.seq; *
 5: /cggn_6/pctdata/1/ina/PCTUS.COMB.seq; *
 6: /cggn_6/pctdata/1/ina/backfiles1.seq; *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	18	100.0	2625 1	US-08-188-228-57
C 2	18	100.0	2625 1	US-08-332-643-51
C 3	18	100.0	2625 1	US-08-332-638-57
C 4	18	100.0	3712 2	US-08-738-349-3
C 5	18	100.0	3914 2	US-08-738-349-5
C 6	16.4	91.1	3581 2	US-08-738-349-1
C 7	15.4	85.6	1014 4	US-09-134-001C-370
C 8	15.4	85.6	2307 3	US-08-942-008-1
C 9	15.4	82.2	38584 4	US-09-455-702B-50
C 10	13.8	76.7	336 2	US-08-606-293-3
C 11	13.8	76.7	336 2	US-08-606-293-7
C 12	13.8	76.7	1065 2	US-08-875-811-10
C 13	13.8	76.7	1055 3	US-08-875-811-48
C 14	13.8	76.7	1074 3	US-08-875-811-44
C 15	13.8	76.7	1074 3	US-08-875-811-50
C 16	13.8	76.7	1086 3	US-08-875-811-46
C 17	13.8	76.7	1137 3	US-08-875-811-42
C 18	13.8	76.7	1299 2	US-08-125-462-6
C 19	13.8	76.7	1299 2	US-08-891-848-6
C 20	13.8	76.7	1320 2	US-08-125-462-3
C 21	13.8	76.7	1320 2	US-08-891-848-3
C 22	13.8	76.7	2100 2	US-08-511-485-9
C 23	13.8	76.7	2691 3	US-08-212-971-9
C 24	13.8	76.7	2691 3	US-08-800-929A-9
C 25	13.8	76.7	2691 4	US-09-617-053A-9
C 26	13.8	76.7	6727 2	US-08-462-2
C 27	13.8	76.7	6727 2	US-08-891-848-2

ALIGNMENTS

RESULT 1
 US-08-188-228-57/C
 ; Sequence 57, Application US/08188228
 ; Patent No. 5597725
 ; GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESS: Bourne
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/188,228
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/049,460
 FILING DATE: 19 APR 1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,643
 FILING DATE: 17 APR 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 5597725and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31340
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2625 base pairs
 STRANDEDNESS: single
 TYPE: nucleic acid
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-188-228-57

Query Match 100.0%; Score 18; DB 1; Length 2625;
 Best Local Similarity 100.0%; Pred. No. 0.56;

RESULT 2
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-08-332-643-51/c
 Patent No. 5339634 Application US/08332643
 GENERAL INFORMATION:
 APPLICANT: Suzuki, shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: Two First National Plaza, 20 South Clark
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/332,643
 FILING DATE: 17 APR 1992
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/07/872,643
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5446250and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31340
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2625 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: cDNA
 US-08-332-638-57

RESULT 3
 Query Match 100.0%; Score 18; DB 1; length 2625;
 Best Local Similarity 100.0%; Pred. No. 0.56; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-08-332-643-51

Query 1 GCGGGCTTGAAAGTA 18
 Db 185 GCGGCGTTGAAACAGTA 168

RESULT 4
 Sequence 3, Application US/08730349
 US-08-730-340-3/c
 General Information:
 Patent No. 5865638
 APPLICANT: Takeshita, Sunao
 APPLICANT: Okazaki, Makoto
 APPLICANT: Kawai, Shinji
 APPLICANT: Tsujimura, Atsushi
 APPLICANT: Amann, Egon
 TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
 TITLE OF INVENTION: Process for Its Production
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/730,349

FILING DATE: 25-OCT-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/364,439
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Barker, M. P.
 REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 02481.1323-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3914 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE: Homo sapiens
 ORGANISM: Homo sapiens
 TISSUE TYPE: Osteosarcoma
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 491..2569
 US-08-738-349-3

Query Match 100.0%; Score 18; DB 2; Length 3712;
 Best Local Similarity 100.0%; Pred. No. 0.58; Mismatches 0;
 Matches 18; Conservative 0; Indels 0; Gaps 0;
 Qy 1 GCGGGCTTGTAACAGTA 18
 Db 490 GCGGGCTTGTAACAGTA 473

RESULT 5
 US-08-738-349-5/c
 Sequence 5, Application US/08738349
 Patent No. 5859638
 GENERAL INFORMATION:
 APPLICANT: Takeshita, Sunao
 APPLICANT: Okazaki, Makoto
 APPLICANT: Kawai, Shinji
 APPLICANT: Tsujimura, Atsushi
 APPLICANT: Amann, Egon
 TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and Process for Its Production
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, Washington, D.C.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3115
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08738,349
 FILING DATE: 25-OCT-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/364,439
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Barker, M. P.
 REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 02481.1323-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3581 base pairs

Query Match 100.0%; Score 18; DB 2; Length 3914;
 Best Local Similarity 100.0%; Pred. No. 0.58; Mismatches 0;
 Matches 18; Conservative 0; Indels 0; Gaps 0;
 Qy 1 GGGGCTTGTAACAGTA 18
 Db 520 GGGGCTTGTAACAGTA 503

RESULT 6
 US-08-738-349-1/c
 Sequence 1, Application US/08738349
 Patent No. 5859638
 GENERAL INFORMATION:
 APPLICANT: Takeshita, Sunao
 APPLICANT: Okazaki, Makoto
 APPLICANT: Kawai, Shinji
 APPLICANT: Tsujimura, Atsushi
 APPLICANT: Amann, Egon
 TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and Process for Its Production
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, Washington, D.C.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3115
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08738,349
 FILING DATE: 25-OCT-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/364,439
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Barker, M. P.
 REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 02481.1323-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3581 base pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: *Mus musculus*
 STRAIN: osteoblastic cell line MC3T3El
 FEATURE: NAME/KEY: CDS
 LOCATION: 284..2571
 US-08-738-349-1

Query Match Best Local Similarity 91.1%; Score 16.4%; DB 2; Length 3581;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GGCAGCTGTAAACGTA 18
 Db 313 GGCAAGCTGTAAACGTA 296

RESULT 7
 Sequence 370, Application US/09134001C
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIORITY NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIORITY APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO: 370
 LENGTH: 1014
 TYPE: DNA
 ORGANISM: *Staphylococcus epidermidis*

US-09-134-001C-370

Query Match Best Local Similarity 85.6%; Score 15.4%; DB 4; Length 1014;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GCGCTGTGATACGTA 18
 Db 692 GCAGCTGTAAACGTA 576

RESULT 8
 US-08-942-008-1

GENERAL INFORMATION:
 Sequence 1, Application US/08942008
 APPLICANT: Bräsemann, Sylvia
 TITLE OF INVENTION: Nucleic Sequences that Encode
 TITLE OF INVENTION: Phosphatidylinositol-3 Kinase Associated Proteins and
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ONYX Pharmaceuticals, Inc.
 STREET: 3031 Research Drive
 CITY: Richmond
 STATE: CA
 COUNTRY: USA
 ZIP: 94806
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/453,702B
 FILING DATE: 03-Dec-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/110,955
 FILING DATE: 04-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-9156

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/942,008
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Giotta, Gregory
 REGISTRATION NUMBER: 32,028
 REFERENCE/DOCKET NUMBER: ONYX1027
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 262-8710
 TELEFAX: (510) 222-9758
 INFORMATION FOR SEO ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2307 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE: NAME/KEY: CDS
 LOCATION: 162..1928
 US-08-942-008-1

Query Match Best Local Similarity 85.6%; Score 15.4%; DB 3; Length 2307;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GGGGCTGTGATACGTA 17
 Db 1153 GGGGGCTGTGATACGTA 1169

RESULT 9
 US-09-433-702B-50
 Sequence 50, Application US/09453702B
 PATENT NO. 6365723
 GENERAL INFORMATION:
 APPLICANT: Blattner, Frederick R.
 Burland, Valerie
 Perina, Nicole T.
 Plunkett, Guy
 Welch, Rod
 TITLE OF INVENTION: No. 6365723el Sequences of *E. coli* 0157
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/453,702B
 FILING DATE: 03-Dec-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/110,955
 FILING DATE: 04-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-9156

INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38594
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLogy: linear
 MOLECULE TYPE: DNA (genomic)

Query Match 82.2%; Score 14.8; DB 4; Length 38584;
 Best Local Similarity 88.9%; Pred. No. 45; Mismatches 0;
 Matches 16; Conservative 0; Indels 0; Gaps 0;
 Qy 1 GGCGGCTGTAACTA 18
 Db 36134 GGCGGCTGTAACTA 36151

RESULT 10
 US-08-606-293-3
 sequence 3, Application US/08606293
 Patent No. 5874082
 GENERAL INFORMATION:
 APPLICANT: de Boer, Mark
 TITLE OF INVENTION: Humanized Anti-CD40 Monoclonal Antibodies and
 FRAGMENTS Capable of Blocking B Cell Activation
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHIRON CORPORATION Intellectual Property - R440
 STREET: 4560 Horton Street, P.O. Box 8097
 CITY: Emeryville
 STATE: California
 COUNTRY: United States of America
 ZIP: 94662-8097

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/606, 293
 FILING DATE:
 CLASSIFICATION: 424
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/070, 158
 FILING DATE: 28-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Saverde, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 27527/33157

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2118
 TELEFAX: (510) 655-3542
 TELEX: n/a

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: Protein
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..336

RESULT 11
 US-08-606-293-7
 Sequence 7, Application US/08606293
 Patent No. 5874082
 GENERAL INFORMATION:
 APPLICANT: de Boer, Mark
 TITLE OF INVENTION: Humanized Anti-CD40 Monoclonal Antibodies and
 FRAGMENTS Capable of Blocking B Cell Activation
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHIRON CORPORATION Intellectual Property - R440
 STREET: 4560 Horton Street, P.O. Box 8097
 CITY: Emeryville
 STATE: California
 COUNTRY: United States of America
 ZIP: 94662-8097

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/606, 293
 FILING DATE:
 CLASSIFICATION: 424
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/070, 158
 FILING DATE: 28-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Saverde, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 27527/33157

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2118
 TELEFAX: (510) 655-3542
 TELEX: n/a

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: Protein
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..336

RESULT 12
 US-08-875-811-40/C
 Sequence 40, Application US/08875811
 Patent No. 6041793
 GENERAL INFORMATION:
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Luis
 APPLICANT: Wlodower, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP

REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1074 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1074
 OTHER INFORMATION: /note= "MetSerOnCAG8FBEG"
 US-08-875-811-44

Query Match 76.7%; Score 13.8; DB 3; Length 1074;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2 GCGGCTGTAAACAGTA 18
Db	907 GCGGGTGTAAATAGTA 891

RESULT 15
 US-08-875-811-50c
 Sequence 50, Application US/08875811
 Patent No. 6045793
 GENERAL INFORMATION:
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Luis
 APPLICANT: Wlodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatientIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY /AGENT INFORMATION:
 NAME: Rais, Susan K.
 REGISTRATION NUMBER: 41,739
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1074 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear

MOLECULE TYPE: DNA
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: 1..1074
 OTHER INFORMATION: /note= "MetGluOncFBEG"
 US-08-875-811-50

Query Match 76.7%; Score 13.8; DB 3; Length 1074;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2 GCGGCTGTAAACAGTA 18
Db	907 GCGGGTGTAAATAGTA 891

Search completed: June 22, 2003, 09:14:29
 Job time : 51 secs

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:44:05 ; search time 142 seconds
(w/without alignments)
186.012 Million cell updates/sec

Title: us-09-830-811-1
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Scoring table: IDENTITY_NUC
Gappen 10.0 , Gapext 1.0

Searched: 1042519 seqs, 73313590 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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11: /cgn2_5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_5/ptodata/2/pubpna/US10_PURCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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C 2	100.0	3867	10	US-09-919-497-5
C 3	85.6	480	9	US-09-918-995-37236
C 4	85.5	7053	10	US-09-9764-864-792
C 5	82.2	142	10	US-09-878-574-9162
C 6	82.2	207	10	US-09-878-574-12381
C 7	82.2	222	10	US-09-878-574-12500
C 8	82.2	249	10	US-09-878-574-11388
C 9	82.2	473	9	US-09-918-995-10360
C 10	82.2	648	10	US-09-974-300-5592
C 11	82.2	1347	9	US-09-938-342A-208
C 12	82.2	30584	9	US-10-11A-170-50
C 13	80.0	229	10	US-09-878-574-8610
C 14	80.0	383	9	US-09-918-995-6449
C 15	80.0	1069	10	US-09-833-381-1732
C 16	80.0	2804	9	US-10-198-846-10399
C 17	80.0	4084	12	US-10-044-090-221
C 18	77.8	297	10	US-09-867-701-10153
C 19	77.8	312	10	US-09-923-876-3656

ALIGMENTS

RESULT 1
US-10-044-090-597/C
; Sequence 597, Application US/10044090
; Patent No. US20020137081AI
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL program
; SEQ ID NO 597
; LENGTH: 3403
; TYPE: DNA
; NAME/KEY: misc_feature
; FEATURE:
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1258943CB1.
; US-10-044-090-597

Query Match Best Local Similarity 100.0%; Score 18; DB 12; Length 3403; Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 GGCGCTTGGTAACAGTA 18
DB 206 GGCGCTTGGTAACAGTA 189

RESULT 2
US-09-919-497-5/C
; Sequence 5, Application US/09919497
; Sequence 10360, A
; Sequence 5592, A
; Sequence 208, A
; Sequence 12381, A
; Sequence 12500, A
; Sequence 11389, A
; Sequence 8610, A
; Sequence 6449, A
; Sequence 1732, A
; Sequence 10399, A
; Sequence 221, A
; Sequence 10153, A
; Sequence 3656, A

GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B001/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31

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; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 5
; LENGTH: 3667
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-919-497-5

Query Match 100.0%; Score 18; DB 10; Length 3867;
Best Local Similarity 100.0%; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Pred. No. 25; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-918-995-37236
Sequence 37236 Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235, 076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 37236
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: NAME/KEY: misc.feature
LOCATION: (1)..(80)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37236

Query Match 85.6%; Score 15 4; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
US-09-764-864-792
Sequence 792 Application US/09764864
Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764, 864
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION DATA removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 792
LENGTH: 7653
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: NAME/KEY: SITE
LOCATION: (154)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-792

Query Match 85.6%; Score 15 4; DB 9; Length 480;
Best Local Similarity 94.1%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 5
US-09-878-574-9162/C
Sequence 9162 Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with Plants
FILE REFERENCE: 38-21(1501)B
CURRENT APPLICATION NUMBER: US/09/878, 574
PRIOR APPLICATION NUMBER: 09/333, 535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO: 9162
LENGTH: 142
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701102155H1
US-09-878-574-9162

Query Match 82.2%; Score 14 8; DB 10; Length 142;
Best Local Similarity 88.9%; Pred. No. 98; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
US-09-878-574-12381/C
Sequence 12381 Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with Plants
FILE REFERENCE: 38-21(1501)B
CURRENT APPLICATION NUMBER: US/09/878, 574
PRIOR APPLICATION NUMBER: 09/333, 535
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO: 12381
LENGTH: 207
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701065703H1
US-09-878-574-12381

Query Match 82.2%; Score 14 8; DB 10; Length 207;
Best Local Similarity 88.9%; Pred. No. 1e-02; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 7
US-01-878-574-12500/C
; Sequence 12500, Application US/09878574
; Patent No. US20020105481
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with FILE REFERENCE: 38-21(1540)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIORITY APPLICATION NUMBER: 09/333, 535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO: 12500
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701065851H1
US-09-878-574-12500

Query Match 82.2%; Score 14.8; DB 10; Length 222;
Best Local Similarity 88.9%; Pred. No. 1.e-02; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGGCTGTAACAGCA 18
Db 164 GGAGGCTGTAAACAGCA 147

RESULT 8
US-09-878-574-11388/C
; Sequence 11388, Application US/09878574
; Patent No. US20020105481
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with FILE REFERENCE: 38-21(1540)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333, 535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO: 11388
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701064387H1
US-09-878-574-11388

Query Match 82.2%; Score 14.8; DB 10; Length 249;
Best Local Similarity 88.9%; Pred. No. 1.1e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGGCTGTAACAGCA 18
Db 167 GGAGGCTGTAAACAGCA 150

RESULT 9
US-03-910-995-10360/C
; Sequence 10360, Application US/0918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS CONA LIBRARIES
; TITLE OF INVENTION: FROM VARIOUS CONA LIBRARIES

Query Match 82.2%; Score 14.8; DB 10; Length 249;
Best Local Similarity 88.9%; Pred. No. 1.1e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGGCTGTAACAGCA 18
Db 167 GGAGGCTGTAAACAGCA 150

RESULT 10
US-09-974-300-5592
; Sequence 5592, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ibm Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene FILE REFERENCE: 10085, 500-US
; CURRENT APPLICATION NUMBER: US/09/974, 300
; CURRENT FILING DATE: 2001-10-05
; PRIORITY APPLICATION NUMBER: 09/680, 598
; PRIOR FILING DATE: 2000-10-06
; PRIORITY APPLICATION NUMBER: 60/279, 526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5592
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-5592

Query Match 82.2%; Score 14.8; DB 10; Length 648;
Best Local Similarity 88.9%; Pred. No. 1.2e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGGCTGTAACAGCA 18
Db 536 GGCCTGTTGAAAGTA 553

RESULT 11
US-09-938-842A-208/C
; Sequence 208, Application US/09938842A
; Patent No. US2001160378A1
; GENERAL INFORMATION:
; APPLICANT: Haiper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT1300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/264,647
 PRIOR FILING DATE: 2001-01-16
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO: 208
 LENGTH: 1347
 TYPE: DNA
 ORGANISM: *Arabidopsis thaliana*
 ; US-09-938-842A-208

RESULT 12
 US-10-114-170-50
 Sequence Match 82.2%; Score 14.8; DB 9; Length 1347;
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 2;
 SEQ ID NO: 1073
 1 GGGGGCTGAAACAGTA 18
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 6GGGGCTGAAACCGGA 1056

RESULT 13
 US-09-878-574-8610/C
 Sequence 8610, Application US/09878574
 Best Local Similarity 93.8%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 2;
 APPLICANT: Blattner, Frederick R.
 Burland, Valerie
 Perrin, Nicole T.
 Plunkett, Guy
 Welch, Rod
 TITLE OF INVENTION: No. US20030023075A1
 NUMBER OF SEQ ID NOS: 1575
 PUBLICATION NO. US20030023075A1
 GENERAL INFORMATION:
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113

COMPUTER READABLE FORM:
 MEDIUM: DISKETTE, 3.50 inch. 1.44Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT SOFTWARE: Word Perfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/114,170
 FILING DATE: 01-APR-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/453,702
 FILING DATE: 03-DEC-1999
 APPLICATION NUMBER: 60/110,955
 FILING DATE: 04-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REFERENCE DOCKET NUMBER: 21386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-9166
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38584
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: Linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 50:
 US-10-114-170-50

Query Match 82.2%; Score 14.8; DB 9; Length 38584;
 ; Sequence 1732, Application US/09833381

Best Local Similarity 88.9%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 SEQ ID NO: 36134
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 6GCCGCGATGAAACAGTA 36151

RESULT 13
 US-09-878-574-8610/C
 Sequence 8610, Application US/09878574
 Best Local Similarity 93.8%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 2;
 APPLICANT: Byrne, Joseph R.
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Thompson, Michael D.
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 38-21(15401)B
 CURRENT APPLICATION NUMBER: US/09/878,574
 CURRENT FILING DATE: 2001-12-21
 PRIOR APPLICATION NUMBER: 09/333,535
 NUMBER OF SEQ ID NOS: 1575
 SEQ ID NO: 8610
 LENGTH: 229
 TYPE: DNA
 ORGANISM: Glycine max
 OTHER INFORMATION: OTHER INFORMATION: Clone ID: 701101435HL
 US-09-878-574-8610

RESULT 14
 US-09-918-995-6449/C
 Sequence 6449, Application US/09918995
 Publication No. US20030073623A1
 GENERAL INFORMATION:
 CURRENT APPLICATION NUMBER: US/09/918,995
 APPLICANT: Hyseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 FILE REFERENCE: 20411-756
 CURRENT APPLICATION NUMBER: US/09/918,995
 PRIOR APPLICATION NUMBER: US/09/235,076
 PRIOR FILING DATE: 1999-01-20
 NUMBER OF SEQ ID NOS: 38054
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 6449
 LENGTH: 383
 TYPE: DNA
 ORGANISM: *Homo sapiens*
 US-09-918-995-6449

Query Match 80.0%; Score 14.4; DB 9; Length 383;
 Best Local Similarity 93.8%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;
 SEQ ID NO: 239
 1 GCGGGCTGAAACAG 16
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 6GCCTGCTGAAACAG 224

RESULT 15
 US-09-833-381-1732/C
 Sequence 1732, Application US/09833381

Patent No. US20020132090A1
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.

TITLE OF INVENTION: No. US20020132090A1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 1732
LENGTH: 1069
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: misc_feature
NAME/KEY: (1)...(1069)
LOCATION: n = A,T,C or G

US-09-833-381-1732
Query March 80.0%; Score 14.4; DB 10; length 1069;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCGGGTTGTAACAG 16
Db 1002 GCGGCCGTCACAG 987

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Job time : 145 secs

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On nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:07:40 ; Search time 2786 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	18	100.0	18 32 US-09-830-811-1	Sequence 1, Appli
2	18	100.0	377 25 US-09-644-871-441B	Sequence 441B, Ap
3	18	100.0	420 16 US-09-293-972-2969	Sequence 2969, A
4	18	100.0	420 34 US-09-904-939-29969	Sequence 29969, A
5	18	100.0	443 16 US-09-287-618-26653	Sequence 26653, A
6	18	100.0	492 31 US-09-824-518-5128	Sequence 5128, A
7	18	100.0	513 20 US-09-534-857-1848	Sequence 1848, Ap
8	18	100.0	619 25 US-09-644-871-7428	Sequence 7428, Ap
9	18	100.0	619 25 US-09-644-871-7428	Sequence 7428, Ap
10	18	100.0	2625 1 PCT-US02-8947-570	Sequence 670, Ap
11	18	100.0	2625 1 PCT-US93-03681-57	Sequence 57, Ap
12	18	100.0	2625 1 PCT-US93-03681-57	Sequence 57, Ap
13	18	100.0	2625 18 US-09-401-441-1	Sequence 1424, Ap
14	18	100.0	2625 18 US-09-442-589-797	Sequence 1424, Ap
15	18	100.0	2625 18 US-09-442-589-797	Sequence 1424, Ap
16	18	100.0	2625 41 US-10-165-818-1	Sequence 1, Appli
17	18	100.0	2625 41 US-10-172-567-570	Sequence 670, Ap
18	18	100.0	3296 30 US-09-770-173-2189	Sequence 2189, Ap
19	18	100.0	3296 30 US-09-770-173-2189	Sequence 2189, Ap
20	18	100.0	3403 38 US-10-044-090-597	Sequence 597, Ap
21	18	100.0	3403 39 US-10-044-090-597	Sequence 597, Ap

RESULT 1
US-09-830-811-1
Sequence 1 Application US/09930811
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
; TITLE OF INVENTION: CADHERIN-11 EXPRESSION, AN ASSAY AND TREATMENT FOR CELLULAR
FILE REFERENCE: 8021-275
CURRENT APPLICATION NUMBER: US/09-830,811
CURRENT FILING DATE: 2001-04-27
PRIORITY FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
S-09-830-811-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 32; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-644-874-1810/c
Sequence 4418 Application US/09644871
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600-1167-001
CURRENT FILING DATE: 2000-08-28
PRIORITY FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9739
SOFTWARE: FastSEQ for Windows Version 4.0

Query Match
Best Local Similarity 100.0%; Score 18; DB 34; Length 420;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-243-972-29969/c
Sequence 4684 Application AP/9362
; Sequence 3024, AP
; Sequence 4684, AP
; Sequence 30189, A
; Sequence 9324, AP
; Sequence 1107, AP
; Sequence 1107, AP
; Sequence 8324, AP
; Sequence 5446, AP
; Sequence 1912, AP
; Sequence 1643, AP
; Sequence 5127, AP
; Sequence 5202, AP
; Sequence 4705, AP
; Sequence 5412, AP
; Sequence 3024, AP
; Sequence 4684, AP
; Sequence 9362, AP

ALIGNMENTS

Query Match
Best Local Similarity 100.0%; Score 18; DB 25; Length 377;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCAGCTGTAACAGTA 18
DB 278 GGCAGCTGTAACAGTA 261

RESULT 4
US-09-904-939-29969/c
Sequence 2969 Application US/09904939
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-769
CURRENT APPLICATION NUMBER: US/09/293,972
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 34258
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29969
LENGTH: 420
TYPE: DNA
ORGANISM: Homo sapiens
US-09-293-972-29969

Query Match
Best Local Similarity 100.0%; Score 18; DB 16; Length 420;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGGGCTGTAAACAGTA 18
DB 380 GCGGGCTGTAAACAGTA 363

Query Match
Best Local Similarity 100.0%; Score 18; DB 34; Length 420;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-644-874-1810/c
Sequence 4418 Application US/09644871
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600-1167-001
CURRENT FILING DATE: 2000-08-28
PRIORITY FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9739
SOFTWARE: FastSEQ for Windows Version 4.0

Query Match
Best Local Similarity 100.0%; Score 18; DB 34; Length 420;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-904-939-29969/c
Sequence 2969 Application US/09904939
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-769
CURRENT APPLICATION NUMBER: US/09/293,972
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 34258
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29969
LENGTH: 420
TYPE: DNA
ORGANISM: Homo sapiens
US-09-904-939-29969

Query Match
Best Local Similarity 100.0%; Score 18; DB 34; Length 420;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-09-287-618-26653/c
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 26653
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..443)
; OTHER INFORMATION: n = A,T,C or G

US-09-287-618-26653

Query Match	Score	DB	Length	Indels	Gaps
Best Local Similarity	100.0%	16	443	0	0
Matches	18;	Conservative	0;	Mismatches	0;

OY 1 GGGGCTTGTAACAGTA 18
Db 427 GCGGCTTGTAAACAGTA 410

RESULT 6
US-09-824-518-5128/c
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600-2078-001
; CURRENT APPLICATION NUMBER: US/09/824,518
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/193,436
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10042
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5128
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-824-518-5128

Query Match	Score	DB	Length	Indels	Gaps
Best Local Similarity	100.0%	15	492	0	0
Matches	18;	Conservative	0;	Mismatches	0;

OY 1 GGGGCTTGTAACAGTA 18
Db 421 GCGGCTTGTAAACAGTA 404

RESULT 8
US-09-644-871-7428/c
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600-1167-001
; CURRENT APPLICATION NUMBER: US/09/644,871
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151,059
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 9739
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7428
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-644-871-7428

Query Match	Score	DB	Length	Indels	Gaps
Best Local Similarity	100.0%	20	619	0	0
Matches	18;	Conservative	0;	Mismatches	0;

OY 1 GGCCTGTTAACAGTA 18
Db 520 GGCGCTTGTAAACAGTA 503

RESULT 7
US-09-534-857-1848/c
; GENERAL INFORMATION:
; APPLICANT: Sellhamer, Jeffrey J.
; APPLICANT: Delegene, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.

US-09-534-857-1848

Query Match	Score	DB	Length	Indels	Gaps
Best Local Similarity	100.0%	31	492	0	0
Matches	18;	Conservative	0;	Mismatches	0;

OY 1 GGCCTGTTAACAGTA 18
Db 27 GCGGCTTGTAAACAGTA 10

RESULT 9
US-09-652-124-7882/c
; Sequence 7882, Application US/09652124
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600-1179-001
; CURRENT APPLICATION NUMBER: US/09/652,124
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,131
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 9868
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7882
; LENGTH: 619
; TYPE: DNA

; ORGANISM: Homo sapiens
; US-09-652-124-7882

; Query Match_i Similarity 100.0%; Score 18; DB 25; Length 619;
; Sequence 670, Application PCT/TUS02/18947
; GENERAL INFORMATION:
; APPLICANT: Rosetta Inpharmatics
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-228
; CURRENT APPLICATION NUMBER: PCT/TUS02/18947
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/310,770

PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 670

LENGTH: 2625
TYPE: DNA

ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESION NUMBER: NM_001797
PCT-US02-18947-670

RESULT 10
PCT-US02-18947-670/C

; Sequence 670, Application PCT/TUS02/18947
; GENERAL INFORMATION:
; APPLICANT: Rosetta Inpharmatics
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-228
; CURRENT APPLICATION NUMBER: PCT/TUS02/18947
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/310,770

PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 670

LENGTH: 2625
TYPE: DNA

ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESION NUMBER: NM_001797
PCT-US02-18947-670

RESULT 11
PCT-US93-03681-57/C

; Sequence 57, Application PCT/TUS9303681
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marisall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; STATE: Illinois
; CITY: Chicago
; ZIP: USA

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03681
FILING DATE: 19930419
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/1872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340

Query Match_i Similarity 100.0%; Score 18; DB 1; Length 2625;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGCTTGAACAGTA 18
Db 185 GCGGGCTTGAACAGTA 168

RESULT 12
US-09-053-175B-1424/C

; Sequence 1424, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chencik, Alex
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B

CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SEQ ID NO 1424
LENGTH: 2625
TYPE: DNA

ORGANISM: Homo sapiens
US-09-053-175B-1424

RESULT 13
US-09-403-441-1/C

; Sequence 1, Application US/09403441
; GENERAL INFORMATION:
; APPLICANT: MacCallum, Colin D
; TITLE OF INVENTION: Cadherin-11 as an Indicator of Viable Pregnancy.
; FILE REFERENCE: 2786/34647
; CURRENT APPLICATION NUMBER: US/09/403,441
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/CA98/00397
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: CA 2,203,718
; PRIOR FILING DATE: 1997-04-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
LENGTH: 2625
TYPE: DNA

ORGANISM: Homo sapiens
US-09-403-441-1

Query Match_i Similarity 100.0%; Score 18; DB 18; Length 2525;
Best Local Similarity 100.0%; Pred. No. 20;
Best Local Similarity 100.0%; Pred. No. 20;
Best Local Similarity 100.0%; Pred. No. 20;

RESULT 14
US-09-442-589B-797/C
Sequence 797, Application US/09442589B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Lukashov, Matvey
TITLE OF INVENTION: Human Cardiovascular Array
FILE REFERENCE: CLON-006CPI0
CURRENT APPLICATION NUMBER: US/09/442,589B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1194
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 97
LENGTH: 2625
TYPE: DNA
ORGANISM: homo sapiens
US-09-442-589B-97

Query Match 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity 100.0%; Score 18; DB 18; Length 2625;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCGGCTTGTAACAGTA	18
Db	185	GCGGCTTGTAACAGTA	168

RESULT 15
US-09-654-328-1/C
Sequence 1, Application US/09654328
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier
TITLE OF INVENTION: Methods and Compositions for Treatment
FILE REFERENCE: B0801/187/ERR/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 2625
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (156)...(2546)
US-09-654-328-1

Query Match 100.0%; Score 18; DB 25; Length 2625;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCGGCTTGTAACAGTA	18
Db	185	GCGGCTTGTAACAGTA	168

Search completed: June 22, 2003, 10:01:12
Job time : 2790 secs

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; RESULT 3
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34245
; Sequence 34246, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34257
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34257

Query Match          100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCGGGCTGTAAACAGTA 18
        ||||||| | | | | | | | | |
Db      37 GCGGCGCTGTAAACAGTA 20

; RESULT 4
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34246
; Sequence 34246, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34246
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34246

Query Match          100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCGGGCTGTAAACAGTA 18
        ||||||| | | | | | | | | |
Db      37 GCGGCGCTGTAAACAGTA 20

; RESULT 5
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34256
; Sequence 34256, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34256
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34256

Query Match          100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCGGGCTGTAAACAGTA 18
        ||||||| | | | | | | | | |
Db      32 GCGGCGCTGTAAACAGTA 15

; RESULT 6
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34258
; Sequence 34258, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34258
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34258

Query Match          100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCGGGCTGTAAACAGTA 18
        ||||||| | | | | | | | | |
Db      37 GCGGCGCTGTAAACAGTA 20

; RESULT 7
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34268
; Sequence 34268, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34268
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-455-444-34268

Query Match          100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCGGGCTGTAAACAGTA 18
        ||||||| | | | | | | | | |
Db      44 GCGGCGCTGTAAACAGTA 27

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RESULT 13
US-60-465-341-34356/2

; ORGANISM: Homo sapiens
US-60-465-241-34258

Sequence No.: 31256 Application US/60465241
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVITCH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLU01458
CURRENT APPLICATION NUMBER: US/60/465 241

CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FastSEQ for Windows Version 4.0

Search completed: June 22, 2003, 10:14:19
Job time: 776 sec

; SEQ ID NO 34256
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
HS-60-465-241-34256

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Qy	Query	Match	Score	DB	Length	Start	End	Similarity	Pred.	No.	Indels	Gaps
1	GGCGGGTGTAAACGTA	18	100.0%	Score 18; DB 13; Length 201; Best Local Similarity 100.0%; Pred. No. 6.1; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.								

RESULT 14
Db 44 GCGGCTGTAAACAGTA 27

RESULT 14

; Sequence 34257, Application US/50465241
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BBOGIVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001468
; CURRENT APPLICATION NUMBER: US/50465, 241
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 258118
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 34257
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-465-241-34257

US-60-465-241-34257

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Query Match          100.0%; Score 18; DB 13; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy . . . . .
  1 GCGGGTTGAAACAGTA 18
  ||||| | | | | | | |
  37 GCGGGTTGAAACAGTA 20
  ||||| | | | | | | |

```

RESULT 15

US-60-465-441-4258-C
; Sequence 34258 Application US/60465241
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/60/465,241
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 218418
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34258
LENGTH: 201
TYPE: DNA

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Om nucleic - nucleic search, using sw model

Run on: June 22, 2003, 08:06:05 ; Search time 1754 seconds
 (without alignments)
 (166.202 Million cell updates/sec)

Title: us-09-830-811-1
Perfect score: 18
Sequence: 1 ggcggcttgtaaacagta 18

Scoring table: IDENTITY_NUC

Searched: 1615406 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_lestba:*
- 2: em_lesthun:*
- 3: em_lestin:*
- 4: em_lestmu:*
- 5: em_lestov:*
- 6: em_lestpl:*
- 7: em_lestro:*
- 8: em_hic:*
- 9: qb_est1:*
- 10: qb_est2:*
- 11: qb_htc:*
- 12: qb_est3:*
- 13: qb_est4:*
- 14: qb_est5:*
- 15: em_estom:*
- 16: em_estfun:*
- 17: qb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	18. 100.0	579 9	AL706659	DKFZp686K1153-r1 686 (synonym: hlcc3) Homo sapiens mRNA linear EST 22-MAR-2002
C 2	18 100.0	585 12	BF194811	DKFZp686K1153 5', mRNA sequence.
C 3	18 100.0	943 9	AU133055	No S1 sequence available.
C 4	18 100.0	960 9	AU133966	This clone (DKFZp686K1153) is available at the RZPD in Berlin.
C 5	18 100.0	964 12	BF33900	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Chaillotteburg, GERMANY; Email: clone@rzpd.de .
C 6	17 94.4	239 9	AA091280	Berlin-Chaillotteburg, GERMANY; Email: clone@rzpd.de . Location/Qualifiers

ALIGNMENTS

RESULT 1
AL708659/c

LOCUS AL708659

DEFINITION DKFZp686K1153-r1 686 (synonym: hlcc3) Homo sapiens mRNA linear EST 22-MAR-2002

ACCESSION DKFZp686K1153

VERSION AL708659.1 GI:19692014

KEYWORDS EST

SOURCE human

ORGANISM Homo sapiens

MATERIALS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 579)

AUTHORS Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.

TITLE EST (Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.)

JOURNAL Unpublished (1999)

COMMENT Contact: Wambutt R

MIPS Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing consortium of the German Genome Project.

No S1 sequence available.

This clone (DKFZp686K1153) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Chaillotteburg, GERMANY; Email: clone@rzpd.de.

FEATURES

ACCESSION AW125499
VERSION AW125499.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus
1 (bases 1 to 384)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 5 (9), 791-806 (1995)
9704477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 435 1706
Fax: 301 443 9890
Email: mbsr@mail.nih.gov
The sequence contained an oligo-dr track that was present in the
oligonucleotide tract that was used to prime the synthesis of first-
strand cDNA and therefore this may represent a bona fide polyA
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dr track served to identify it as a clone from the
normalized brain stems library cDNA library Preparation: M.B.
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq Primer: M13 Forward
SEQ_PRIMER: YES
LocateOnQualifiers

1. .384

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/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="vector: PT713D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI. The
NIH_BMAP_M_S3.2 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged, normalized libraries from ten regions of the mouse
brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hippocampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated. The following
process: NIH_BMAP_M_S3.2, NIH_BMAP_M_S2, NIH_BMAP_M_S1.
The subtracted library (NIH_BMAP_M_S3.2) was constructed
as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S2
clones from which 3' ESTs had been derived was used as a
driver in a hybridization with the NIH_BMAP_M_S2 library
in the form of single stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxypatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (LifeTechnologies) to generate the
NIH_BMAP_M_S3.2 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)
TAG LIB=NIH_BMAP_M_S3.2
TAG TISSUE=brain-stems
TAG_SEQ=TCAG"

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TITLE	A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watani,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. et al.	REFERENCE AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)	COMMENT	Unpublished (2001)
COMMENT	Contact: Yoshihide Hayashizaki		Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 URL: http://genome.gsc.riken.go.jp/ Email: genome-res@gsc.riken.go.jp/
FEATURES	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res.: 10 (10), 1617-1630 (2000)	COMMENT	Carinici,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
source	wagi,K., Fujisawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Itoneda,Y., Ishikawa,T., Ozawa,T., Tanaka,T., Matsumura S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.		Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res.: 10 (10), 1617-1630 (2000)
SEQUENCING PIPELINE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res.: 10 (11), 1757-1771 (2000)	COMMENT	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res.: 11 (2), 281-289 (2001)
FEATURES	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res.: 10 (11), 1757-1771 (2000)	COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
source			e mouse tissues.
LOCATION/QUALIFIERS	Location/Qualifiers		
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/note="pooled tissues ; (tissue_type=cerebellum, dev_stage=16 days neonate, sex=mixed), (tissue_type=cerebellum, dev_stage=0 day neonate, sex=mixed), (tissue_type=hippocampus, dev_stage=adult, sex=male), (tissue_type=whole body, dev_stage=9 days embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days embryo, sex=mixed)"			
BASE COUNT	135 a 98 c 145 g	ORIGIN	101 t
ORIGIN			
QUERY	Query Match		
Best Local Similarity	91.1%	Score	16.4;
Matches	94.4%;	DB	10;
Best Local Similarity	94.4%;	Length	479;
Matches	17;	Indels	1;
Qy	GGCGGTGAAACAGTA 18	Mismatches	0;
Db	323 GGCAGCTTGAAACAGTA 306	Gaps	0;
RESULT	12		
ACCESSION	A139134	LOCUS	A139134/c
DEFINITION	mb72907.y1 Soares mouse p3NMR19.5 Mus musculus cDNA clone IMAGE:35005 5' similar to gb:x77557 M.musculus cad1 mRNA (MOUSE);, mRNA sequence.	VERSION	mb72907.y1 Soares thymus_2kbM7 Mus musculus cDNA clone IMAGE:126293 5' similar to gb:D31963 Mouse mRNA for cadherin-11 (MOUSE);, mRNA sequence.
VERSION	A139134	KEYWORDS	AA839644
KEYWORDS	A139134.1 GI:4217341	SOURCE	AA839644.1 GI:2915739
ORGANISM	Mus musculus		
REFERENCE	Bukarvata; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammal; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. (bases 1 to 501)	AUTHORS	1 (bases 1 to 501)
REFERENCE	Marra,M., Hillier,L., Kucaba,T., Steptoe,B., Theising,B., Martin,J., Beck,C., Wyllie,T., B., Swaller,T., Gibbons,M., Pope,D., Harvey,N., Schurk,R., Ritter E., Kohn,S., Shin,I., Jackson,T., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.	AUTHORS	Marra,M., Hillier,L., Kucaba,T., Steptoe,B., Theising,B., Martin,J., Beck,C., Wyllie,T., B., Swaller,T., Gibbons,M., Pope,D., Harvey,N., Schurk,R., Ritter E., Kohn,S., Shin,I., Jackson,T., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus		
ORGANISM			Helsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Moore,B.,

TITLE	
The Watson-HM1 Mouse EST Project	
JOURNAL	
Unpublished (1996)	
COMMENT	
Wastu-HM1 Mouse EST Project	
Washington University School of Medicine	
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
Contact: Marra M/Mouse EST Project	
Tel: 314 286 1800	
Fax: 314 286 1810	
Email: mouseest@watsen.wustl.edu	
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.	
. MG:6654B8	
Seq primer: -28m13 rev2 ET from Amersham	
High quality sequence stop: 312.	
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was primed with a Not I - oligo(dT) primer [5'-	
GTTTACCACTCTAAGGGGGCGCTTTTTTTTTTTTTTTTTTTTT-	
3'] double-stranded cDNA was ligated to Eco RI adaptors	
(Pharmacia) digested with Not I and cloned into the Not I	
and Eco RI sites of the modified pRT3 vector. RNA	
provided by Dr. Bertrand Jordan. Library went through two	
rounds of normalization, and was constructed by Benito	
Soares and M.Fatima Bonaldo."	
152 a 119 c 119 g 111 t	
BASE COUNT	
ORIGIN	
Query Match 91.1%; Score 16.4; DB 9; Length 501;	
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polylinker; Site_1: Not I; Site_2: Eco RI; The following	
clones from which 3' ESTs had been derived was used as a	
series, ultimately derived from a mixture of individually	
tagged normalized libraries from ten regions of the mouse	
brain (cerebellum, brain stems, olfactory bulbs,	
hypothalamus, cortex, amygdala, basal ganglia, pineal	
gland, striatum, hippocampus) after a series of	
subtractions to reduce the representation of cDNAs from	
which ESTs had already been generated. The following	
process: NIH_BMAP_M_S3.2, NIH_BMAP_M_S2, NIH_BMAP_M_S1.	
The subtracted library (NIH_BMAP_M_S3.2) was constructed	
as follows: paramolified cDNA inserts from NIH_BMAP_M_S2	
clones from which 3' ESTs had been derived was used as a	
driver in a hybridization with the NIH_BMAP_M_S2 library	
in the form of single-stranded circles. The remaining	
single-stranded circles (subtracted library) was purified	
by hydroxypapite column chromatography, converted to	
double-stranded circles and electroporated into DH10B	
bacteria (LifeTechnologies) to generate the	
NIH_BMAP_M_S3.2 library. This procedure has been	
previously described (Bonaldo, Lennon and Soares, Genome	
Research 6:791-806, 1996).	
FEATURES	
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polylinker; Site_1: Not I; Site_2: Eco RI; The following	
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Research 6:791-806, 1996).	
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polylinker; Site_1: Not I; Site_2: Eco RI; The following	
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hypothalamus, cortex, amygdala, basal ganglia, pineal	
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bacteria (LifeTechnologies) to generate the	
NIH_BMAP_M_S3.2 library. This procedure has been	
previously described (Bonaldo, Lennon and Soares, Genome	
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FEATURES	
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polylinker; Site_1: Not I; Site_2: Eco RI; The following	
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series, ultimately derived from a mixture of individually	
tagged normalized libraries from ten regions of the mouse	
brain (cerebellum, brain stems, olfactory bulbs,	
hypothalamus, cortex, amygdala, basal ganglia, pineal	
gland, striatum, hippocampus) after a series of	
subtractions to reduce the representation of cDNAs from	
which ESTs had already been generated. The following	
process: NIH_BMAP_M_S3.2, NIH_BMAP_M_S2, NIH_BMAP_M_S1.	
The subtracted library (NIH_BMAP_M_S3.2) was constructed	
as follows: paramolified cDNA inserts from NIH_BMAP_M_S2	
clones from which 3' ESTs had been derived was used as a	
driver in a hybridization with the NIH_BMAP_M_S2 library	
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single-stranded circles (subtracted library) was purified	
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NIH_BMAP_M_S3.2 library. This procedure has been	
previously described (Bonaldo, Lennon and Soares, Genome	
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FEATURES	
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polylinker; Site_1: Not I; Site_2: Eco RI; The following	
clones from which 3' ESTs had been derived was used as a	
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The subtracted library (NIH_BMAP_M_S3.2) was constructed	
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clones from which 3' ESTs had been derived was used as a	
driver in a hybridization with the NIH_BMAP_M_S2 library	
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by hydroxypapite column chromatography, converted to	
double-stranded circles and electroporated into DH10B	
bacteria (LifeTechnologies) to generate the	
NIH_BMAP_M_S3.2 library. This procedure has been	
previously described (Bonaldo, Lennon and Soares, Genome	
Research 6:791-806, 1996).	
FEATURES	
source	
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polylinker; Site_1: Not I; Site_2: Eco RI; The following	
clones from which 3' ESTs had been derived was used as a	
series, ultimately derived from a mixture of individually	
tagged normalized libraries from ten regions of the mouse	
brain (cerebellum, brain stems, olfactory bulbs,	
hypothalamus, cortex, amygdala, basal ganglia, pineal	
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The subtracted library (NIH_BMAP_M_S3.2) was constructed	
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single-stranded circles (subtracted library) was purified	
by hydroxypapite column chromatography, converted to	
double-stranded circles and electroporated into DH10B	
bacteria (LifeTechnologies) to generate the	
NIH_BMAP_M_S3.2 library. This procedure has been	
previously described (Bonaldo, Lennon and Soares, Genome	
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FEATURES	
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clones from which 3' ESTs had been derived was used as a	
series, ultimately derived from a mixture of individually	
tagged normalized libraries from ten regions of the mouse	
brain (cerebellum, brain stems, olfactory bulbs,	
hypothalamus, cortex, amygdala, basal ganglia, pineal	
gland, striatum, hippocampus) after a series of	
subtractions to reduce the representation of cDNAs from	
which ESTs had already been generated. The following	
process: NIH_BMAP_M_S3.2, NIH_BMAP_M_S2, NIH_BMAP_M_S1.	
The subtracted library (NIH_BMAP_M_S3.2) was constructed	
as follows: paramolified cDNA inserts from NIH_BMAP_M_S2	
clones from which 3' ESTs had been derived was used as a	
driver in a hybridization with the NIH_BMAP_M_S2 library	
in the form of single-stranded circles. The remaining	
single-stranded circles (subtracted library) was purified	
by hydroxypapite column chromatography, converted to	
double-stranded circles and electroporated into DH10B	
bacteria (LifeTechnologies) to generate the	
NIH_BMAP_M_S3.2 library. This procedure has been	
previously described (Bonaldo, Lennon and Soares, Genome	
Research 6:791-806, 1996).	
FEATURES	
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polylinker; Site_1: Not I; Site_2: Eco RI; The following	
clones from which 3' ESTs had been derived was used as a	
series, ultimately derived from a mixture of individually	
tagged normalized libraries from ten regions of the mouse	
brain (cerebellum, brain stems, olfactory bulbs,	
hypothalamus, cortex, amygdala, basal ganglia, pineal	
gland, striatum, hippocampus) after a series of	
subtractions to reduce the representation of cDNAs from	
which ESTs had already been generated. The following	
process: NIH_BMAP_M_S3.2, NIH_BMAP_M_S2, NIH_BMAP_M_S1.	
The subtracted library (NIH_BMAP_M_S3.2) was constructed	
as follows: paramolified cDNA inserts from NIH_BMAP_M_S2	
clones from which 3' ESTs had been derived was used as a	
driver in a hybridization with the NIH_BMAP_M_S2 library	
in the form of single-stranded circles. The remaining	
single-stranded circles (subtracted library) was purified	
by hydroxypapite column chromatography, converted to	
double-stranded circles and electroporated into DH10B	
bacteria (LifeTechnologies) to generate the	
NIH_BMAP_M_S3.2 library. This procedure has been	
previously described (Bonaldo, Lennon and Soares, Genome	
Research 6:791-806, 1996).	
FEATURES	
source	
1. .509	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/	

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mst@mail.nih.gov
 Oligo dt track not found. Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA library preparation: M.B.
 Soares Lab clone distribution: Researchers may obtain BMAP cDNA
 clones from RESEARCH GENETICS. It should be noted that Bent Soares
 is generating a small number of additional specialized
 non-redundant arrays of BMAP cDNAs whose availability will be
 considered under appropriate and limited collaborative arrangements
 Seq primer: M13 Forward
 POLYA=No.

FEATURES SOURCE Location/Qualifiers

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/strain="C57BL/6J"

/db_xref="taxon:0090"

/clone_id="MCG0P_bp_c-07-0-UI"

/lab_host="DIBI0B (Life Technologies)"

/note="vector: p7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NIH_BMAP_Reta_S2 library is a subtracted library,
 ultimately derived from mouse retina tissue libraries at
 various stages of development. For a detailed description
 of the library from which this clone was derived, please
 visit our web site at brainest.eng.uiowa.edu. The tissue
 for this library was contributed by Dr. Xin-Yuan Fu, Yale
 University School of Medicine
 TAG_SEQ=None found"

121 a .158 c 124 g 136 t

BASE COUNT

ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 539;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GCGGGCTTGAAACAGTA 18
 Db 295 GGCAGCTTGTAAACAGTA 312

Search completed: June 22, 2003, 09:13:30

Job time : 1761 secs